



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Selifonov et al

Application No.: 09/539,486

Filed: March 30, 2000

Title: METHOD FOR MAKING CHARACTER  
STRINGS, POLYNUCLEOTIDES AND  
POLYPEPTIDES HAVING DESIRED  
CHARACTERISTICS

Attorney Docket No.:  
MXGNP001X2/0124.510

Examiner: Not yet assigned

Group: 1651

1151  
\$  
#33  
AP  
3-27-03

RECEIVED

MAR 21 2003

TECH CENTER 1600/2900

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the  
United States Postal Service as First Class Mail to: Commissioner for  
Patents, Washington, DC 20231 on March 12, 2003.

Signed: *Leslie Russell*

Leslie Russell

**INFORMATION DISCLOSURE STATEMENT  
BEFORE FINAL ACTION OR NOTICE OF ALLOWANCE  
(37 CFR §§ 1.56 AND 1.97(c))**

Commissioner for Patents  
Washington, DC 20231

Dear Sir:

The references listed in the attached PTO Form 1449 may be material to examination of the above-identified patent application. Applicants submit the list of these references in compliance with their duty of disclosure pursuant to 37 CFR §§1.56 and 1.97. The Examiner is requested to make these references of official record in this application. The above-identified application is a continuation in part of prior application U.S. Patent Application No. 09/494,282. This prior application is being relied upon for an earlier filing date under 35 U.S.C. § 120. Because the listed references were either cited by the PTO, or submitted to the PTO in the prior application, under 37 CFR § 1.98(d) Applicants submit that copies need not be provided.

This Information Disclosure Statement is not to be construed as a representation that a search has been made, that additional information material to the examination of this application does not exist, or that this reference indeed constitutes prior art.

This Information Disclosure Statement is being filed after the mailing date of the first Office Action on the merits, or after three months of the filing date of this application, whichever event occurred last, but it is believed before the mailing date of either: (i) a final action under §1.113 or (ii) a notice of allowance under §1.311, whichever occurs first.

Accompanying this Information Disclosure Statement is

- ☐ a statement as specified in 37 CFR 1.97(e); or
- ☒ the fee set forth in 37 CFR 1.17(p).

If fees are due, enclosed is our Check No. 7007 for \$180.00 in payment of the Information Disclosure Statement Fee. If it is determined that any additional fees are due, the Commissioner is hereby authorized to charge such fees to Deposit Account 500388 (Order No. MXGNP001X2).

Respectfully submitted,

BEYER WEAVER & THOMAS, LLP



Jeffrey K. Weaver  
Registration No. 31,314

P.O. Box 778  
Berkeley, CA 94704-0778  
(510) 843-6200



<b>Form 1449 (Modified)</b>  <b>Information Disclosure Statement By Applicant</b>  (Use Several Sheets if Necessary)	Atty Docket No. <b>MXGNP001X2</b>	Application No.: <b>09/539,486</b>
	Applicant: <b>Selifonov et al.</b>	Group <b>1651</b>
	Filing Date <b>March 30, 2000</b>	

#### U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1	6,125,331	9/26/00	Toh			
	A2	6,403,312	6/11/02	Bassil, et al			
	A3						

#### Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1	WO00/47612	8/17/00	WIPO				
	B2	WO01/61344	8/23/01	WIPO				
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO				

#### Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," <i>Protein Science</i> 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," <i>Protein Science</i> , 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," <i>Protein Science</i> , 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," <i>Journal of Cellular Biochemistry Supplement</i> , 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," <i>Int. J. Peptide Protein Res.</i> 37:414-427 (1991)
	C6	Martin van Heel, "A New Family of Powerful Multivariate Statistical Sequence Analysis Techniques," <i>J. Mol. Biol.</i> , 220:877-887 (1991)
	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," <i>Drug Dev. Research</i> 33:125-132 (1994)
	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," <i>J. Mol. Recognit.</i> 14:308-314 (2001)

**RECEIVED**

MAR 21 2003

TECH CENTER 1600/2900



<b>Form 1449 (Modified)</b>  <b>Information Disclosure Statement By Applicant</b>  (Use Several Sheets if Necessary)	Atty Docket No. <b>MXGNP001X2</b> Applicant: <b>Selifonov et al.</b> Filing Date <b>March 30, 2000</b>	Application No.: <b>09/539,486</b>  Group <b>1651</b>
--	---	---

C9	Miyazawa et al., "Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading," J. Mol. Biol., 256:623-644 (1996)
C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
C11	Miyazawa et al., "Self-Consistent Estimation of Inter-Residue Protein Contact Energies Based on an Equilibrium Mixture Approximation of Residues," Proteins: Structure, Function, and Genetics, 34:49-68 (1999)
C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
C16	H.W. Hellinga, "Rational Protein Design: Combining Theory and Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
C17	William F. DeGrado, "Proteins from Scratch," Science, Vol. 278, 80-81 (1997)
C18	Goldman, "An Algorithmically Optimized Combinatorial Library Screened by Digital Imaging Spectroscopy," Biotechnology (NY), (12):1557-61, 1992
C19	Youvan, "Imaging Sequence Space," Nature 1994, 369(6475):79-80
C20	Harayama, Shigeaki, "Artificial Evolution by DNA Shuffling," Tibtech vol. 16 pp 76-82, 1998
C21	Stemmer, "DNA Shuffling by Random Fragmentation and Reassembly: In vitro Recombination for Molecular Evolution," Proc. Natl. Acad. Sci. USA vol. 91 pp 10747-70751, 1994
C22	Singh et al., "Application of Genetic Algorithms to Combinatorial Synthesis: A Computational Approach to Lead Identification and Lead Optimization," J. Chem. Inf. Compit. Sci vol. 118 pp 1669-1676, 1996

RECEIVED

Pg. 2 of 3

MAR 21 2003

TECH CENTER 1600/2900



<b>Form 1449 (Modified)</b>  <b>Information Disclosure Statement By Applicant</b>  (Use Several Sheets if Necessary)	Atty Docket No. <b>MXGPN001X2</b>	Application No.: <b>09/539,486</b>
	Applicant: <b>Selifonov et al.</b>	Group <b>1651</b>
	Filing Date <b>March 30, 2000</b>	

	C23	Zhang, Ching, "A Genetic Algorithm for Molecular Sequence Comparison," Proceedings of the International Conference on the Systems, Man and Cybernetics
	C24	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C25	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In <i>Escheruchua coli</i> Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C26	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C27	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
	C28	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)
	C29	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C30	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122. November1994
	C31	Moore et al., <u>Modeling and Optimization of DNA Recombination</u> , Computer and Chemical Engineering 2000, Department of Chemical Engineering, The Pennsylvania State University, University Park © 2000
	C32	Gregory L. Moore, Costas D. Maranas, <u>Modeling DNA Mutation and Recombination for Directed Evolution Experiments</u> , Department of Chemical Engineering, The Pennsylvania State University, University Park. Received 28. October 1999. Accepted in revised form 15 April 2000 © 2000 Academic Press
Examiner		Date Considered

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.